

Mapk13 Cas9-KO Strategy

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Project Overview

Project Name

Mapk13

Project type

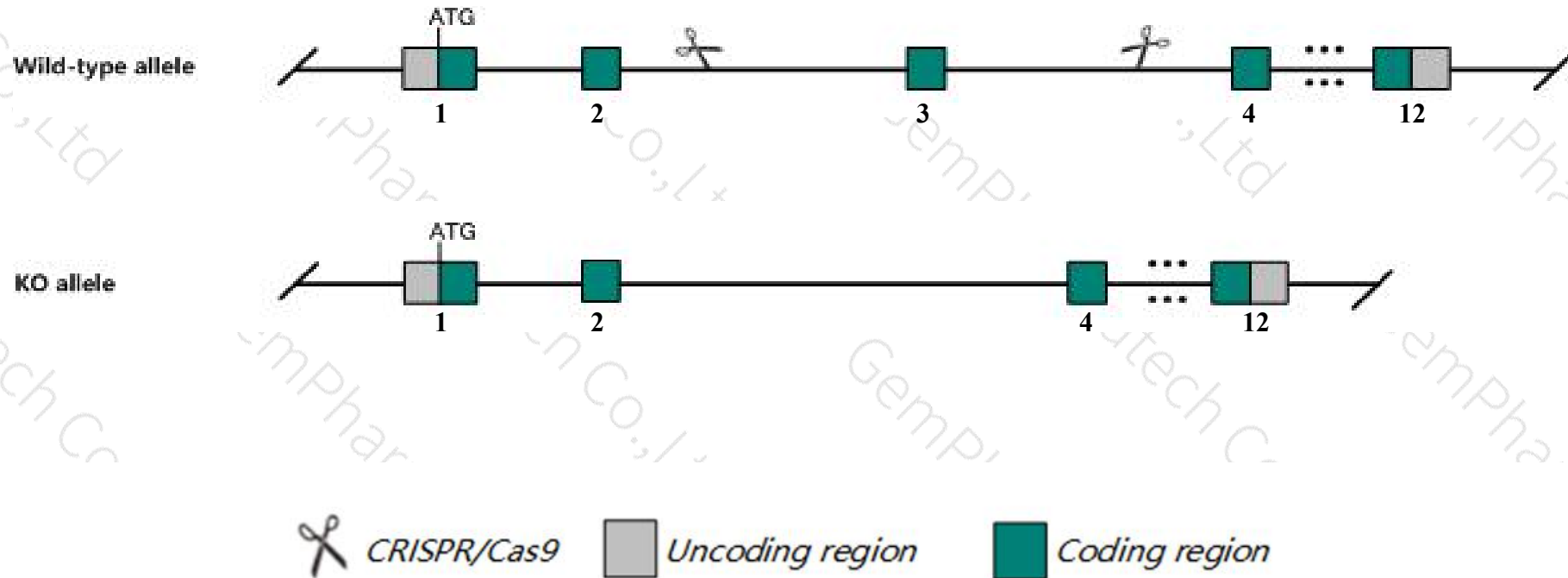
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mapk13* gene. The schematic diagram is as follows:



- The *Mapk13* gene has 9 transcripts. According to the structure of *Mapk13* gene, exon3 of *Mapk13-209* (ENSMUST00000233984.1) transcript is recommended as the knockout region. The region contains 59bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mapk13* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele exhibit improved glucose tolerance, increased insulin secretion, decreased blood glucose, and decreased susceptibility to diet- or chemically-induced diabetes.
- The *Mapk13* gene is located on the Chr17. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Mapk13 mitogen-activated protein kinase 13 [*Mus musculus* (house mouse)]

Gene ID: 26415, updated on 12-Aug-2019

Summary

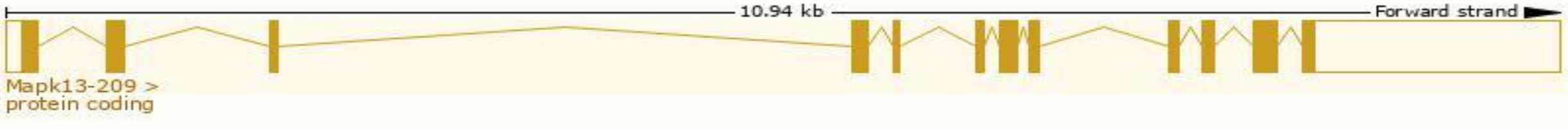
Official Symbol	Mapk13 provided by MGI
Official Full Name	mitogen-activated protein kinase 13 provided by MGI
Primary source	MGI:MGI:1346864
See related	Ensembl:ENSMUSG000000004864
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	SAPK4; Serk4
Expression	Biased expression in large intestine adult (RPKM 152.1), colon adult (RPKM 106.2) and 9 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mapk13-209	ENSMUST00000233984.1	2937	366aa	Protein coding	CCDS28584	Q3UIB2 Q9Z1B7	GENCODE basic APPRIS P1
Mapk13-201	ENSMUST00000004986.13	1526	308aa	Protein coding	-	-	CDS 5' incomplete TSL:1
Mapk13-206	ENSMUST00000233109.1	825	266aa	Protein coding	-	A0A3B2WAS4	CDS 3' incomplete
Mapk13-207	ENSMUST00000233460.1	621	186aa	Protein coding	-	A0A3B2W3M0	CDS 3' incomplete
Mapk13-203	ENSMUST00000129096.2	1830	257aa	Nonsense mediated decay	-	D6RG58	TSL:5
Mapk13-208	ENSMUST00000233676.1	1127	227aa	Nonsense mediated decay	-	A0A3B2WBB9	
Mapk13-205	ENSMUST00000233051.1	864	40aa	Nonsense mediated decay	-	A0A3B2WBD8	
Mapk13-204	ENSMUST00000133786.2	815	62aa	Nonsense mediated decay	-	A0A3B2WDA4	TSL:3
Mapk13-202	ENSMUST00000124099.7	1177	No protein	Retained intron	-	-	TSL:5

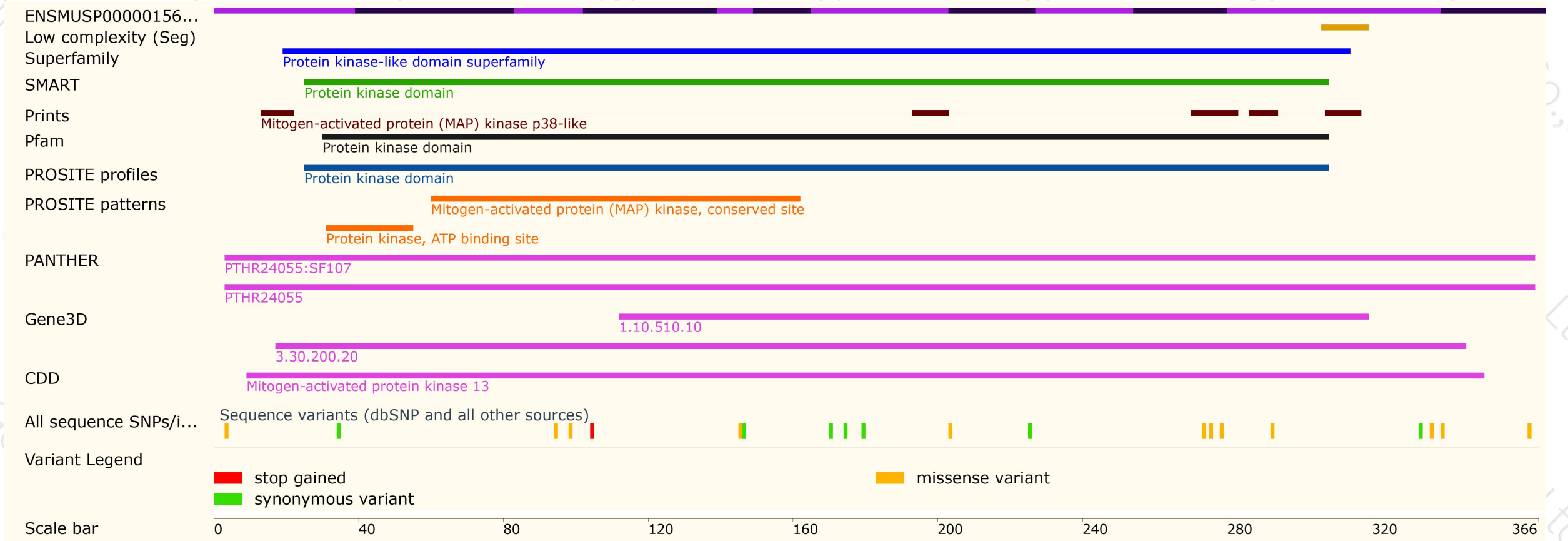
The strategy is based on the design of *Mapk13-209* transcript,The transcription is shown below



Genomic location distribution

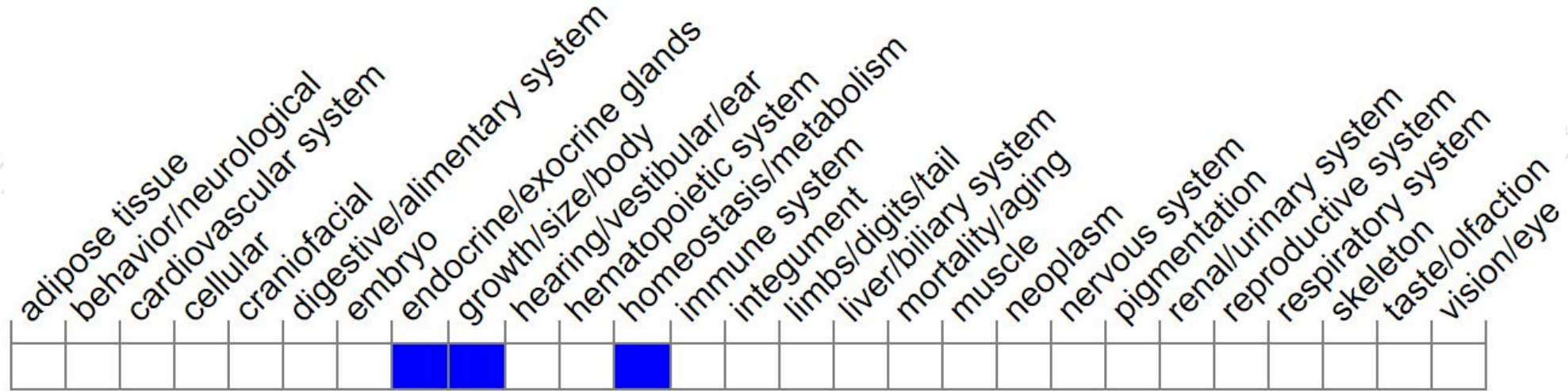


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview ?



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

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If you have any questions, you are welcome to inquire.

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